

STN Search Summary
09/963790

=> d his

FILE 'CAPLUS' ENTERED AT 16:25:47 ON 04 DEC 2003

L1 313 S DEAD (S) HELICASE

L2 2 S L1 AND (CORYNEFORM OR GLUTAMICUM)

L3 1035524 S 1-2

L2 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2003:376895 CAPLUS

DN 138:380486

TI Corynebacterium SES (genetic stability, gene expression and protein secretion) genes and their use for enhancing production of fine chemicals

IN Zelder, Oskar; Pompejus, Markus; Schroeder, Hartwig; Kroeger, Burkhard; Klopprogge, Corinna; Haberhauer, Gregor

PA BASF Aktiengesellschaft, Germany

SO PCT Int. Appl., 265 pp.

CODEN: PIXXD2

DT Patent

LA German

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003040180	A2	20030515	WO 2002-EP12138	20021031
	DE 10154180	A1	20030515	DE 2001-10154180	20011105
PRAI	DE 2001-10154180	A	20011105		

L2 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2002:256307 CAPLUS

DN 136:293612

TI Sequence of dead gene from corynebacteria and use thereof in synthesis of L-lysine

IN Farwick, Mike; Huthmacher, Klaus; Brehme, Jennifer; Pfefferle, Walter

PA Degussa A.-G., Germany

SO PCT Int. Appl., 52 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002026787	A1	20020404	WO 2001-EP10772	20010918
	DE 10047865	A1	20020418	DE 2000-10047865	20000927
	AU 2001093821	A5	20020408	AU 2001-93821	20010918
	EP 1320544	A1	20030625	EP 2001-974264	20010918
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	US 2002115161	A1	20020822	US 2001-963790	20010927
PRAI	DE 2000-10047865	A	20000927		
	WO 2001-EP10772	W	20010918		

SEQUENCE SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 17:12:34 ; Search time 8732 Seconds
(without alignments)
11155.041 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

WD 02/26787

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2381	100.0	2381	6	AX404864	Sequence
	2	2377.8	99.9	333150	1	AP005277	Corynebac
	3	2377.8	99.9	349980	6	AX127146	Sequence
	4	2377.8	99.9	349980	6	AX127147	Sequence
	5	2126.8	89.3	2196	6	AX121362	Sequence
	6	2126.8	89.3	2196	6	BD163479	Novel pol
	7	1498.4	62.9	308650	1	AP005218	Corynebac
	8	590.6	24.8	11785	1	AE012833	Chlorobiu
c	9	583.6	24.5	12009	1	AE011922	Xanthomon
c	10	574.2	24.1	10101	1	AE012376	Xanthomon
	11	563.8	23.7	17916	1	AE007004	Mycobacte
	12	563.8	23.7	36030	1	MTCY50	Z77137 Mycobacteri
	13	563.8	23.7	75216	6	AX704275	Sequence
	14	562.2	23.6	299450	1	BX248338	Mycobacte
	15	545	22.9	2333	1	KPNDEAD	L08387 Klebsiella
c	16	519.8	21.8	300029	1	AE012553	Xylella f
c	17	519.6	21.8	12008	1	AE003878	Xylella f
c	18	516	21.7	11002	1	AE015331	Shigella
c	19	516	21.7	292497	1	AE016989	Shigella
c	20	516	21.7	300359	1	AE016767	Escherich
c	21	514.6	21.6	14820	1	AE000397	Escherich
c	22	514.6	21.6	14820	6	AX370215	Sequence
c	23	514.6	21.6	14820	6	AX370260	Sequence
c	24	514.6	21.6	110000	1	ECOUW67_0	U18997 Escherichia
c	25	513.6	21.6	110000	2	AC074221_3	Continuation (4 of
c	26	511.4	21.5	20120	1	AE008851	Salmonell
c	27	508	21.3	10994	1	AE005544	Escherich
c	28	508	21.3	307962	1	AP002564	Escherich
	29	500.8	21.0	2863	6	BD103627	Method an
c	30	500.2	21.0	258050	1	AL627278	Salmonell
c	31	500.2	21.0	301574	1	AE016844	Salmonell
	32	497.2	20.9	2982	1	ECODEAD	M63288 E.coli dead
c	33	468.6	19.7	11873	1	AE004710	Pseudomon

OM nucleic - nucleic search, using sw model

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2381	100.0	2381	24	AAD28043	Apple. 410 Corynebacterium gl
	2	2377.8	99.9	349980	22	AAH68527	EP C glutamicum codin
	3	2377.8	99.9	349980	22	AAH68528	EP C glutamicum codin
	4	2126.8	89.3	2196	22	AAH66243	EP C glutamicum codin
	5	1674	70.3	1674	25	ACA00444	DE 10/28510 - lots of seg C. glutamicum deri
	6	563.8	23.7	75216	24	ABX09141	Mycobacterium tube
	7	563.8	23.7	4403765	22	AAI99683	Mycobacterium tube
	8	563.8	23.7	4411529	22	AAI99682	Mycobacterium tube
	9	514.6	21.6	1941	23	AAS52577	E. coli DNA for ce
c	10	514.6	21.6	14820	22	AAS46246	DNA encoding novel
c	11	514.6	21.6	14820	22	AAS46268	DNA encoding novel
	12	500.8	21.0	2863	19	AAV38314	Nucleotide sequenc
	13	500.2	21.0	1941	23	AAS56034	Salmonella typhi D
	14	468.4	19.7	1704	23	AAS54151	Pseudomonas aerugi
	15	445.4	18.7	3020	23	AAS89058	DNA encoding novel
c	16	442.6	18.6	1219	23	AAS81866	DNA encoding novel
	17	357.6	15.0	1842	23	AAS53256	Haemophilus influe
	18	357.6	15.0	1830121	17	AAT42063	Haemophilus influe
c	19	295.8	12.4	640681	24	ABA92787	Buchnera sp. genom
	20	271.4	11.4	1536	24	AAD31864	Lactobacillus rham
	21	269.2	11.3	1800	20	AAZ25012	Lactobacillus reut
	22	262	11.0	273	25	ACA00443	C. glutamicum deri
	23	259.4	10.9	5738	24	ABQ70978	Listeria monocytog
	24	253	10.6	1163020	24	ABQ67197	Listeria innocua c
	25	253	10.6	2944528	24	ABA03041	Listeria monocytog
	26	253	10.6	3011208	24	ABQ69245	Listeria innocua D
	27	244.8	10.3	1617	24	ABN69410	Streptococcus poly
	28	242.6	10.2	2365589	24	ABA90521	Genomic sequence o
	29	235.4	9.9	1575	23	AAS55756	Streptococcus pneu
	30	234.6	9.9	1618	18	AAT62139	Leishmania brazili
	31	234.4	9.8	939	24	ABK74369	Bacillus lichenifo
	32	233.8	9.8	1572	25	ABX07336	S. pneumoniae type
	33	233.8	9.8	1638	25	ABZ42472	Streptococcus pneu
c	34	233.8	9.8	3230	19	AAV52336	Streptococcus pneu
c	35	233.8	9.8	2162598	25	ABS56454	Streptococcus pneu
	36	233	9.8	1618	16	AAT05503	Leishmania sp. ant
	37	233	9.8	1618	18	AAT80384	DNA encoding LbeIF
	38	233	9.8	1618	19	AAV47559	Leishmania antigen
	39	233	9.8	1618	20	AAX02202	L. braziliensis EI
	40	233	9.8	1618	24	AAD47112	Leishmania sp. LeI
	41	233	9.8	1618	24	AAF88525	L. braziliensis Lb
	42	233	9.8	1618	24	AAD40286	Leishmania brazili
	43	233	9.8	1618	24	ABK81734	Leishmania antigen
	44	233	9.8	1618	24	AAS96023	Leishmania antigen
	45	223	9.4	1867	18	AAT80385	DNA encoding LmeIF

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

```
Run on:      October 14, 2003, 19:06:09 ; Search time 4971 Seconds
              (without alignments)
              11641.311 Million cell updates/sec
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```
Title:          US-09-963-790A-1
Perfect score: 2381
Sequence:      1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

Database :
EST:*
1:  em_estba:*
2:  em_esthum:*
3:  em_estin:*
4:  em_estmu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
9:  gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

```

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	241	10.1	3539	28	BH770982		BH770982	LLMGtag70
	2	213.2	9.0	1101	29	BZ549647		BZ549647	pacs1-60_
	3	195.4	8.2	1443	12	BM321064		BM321064	rockefell
	4	193.6	8.1	1929	11	AY104966		AY104966	Zea mays
c	5	190.6	8.0	936	29	BZ566692		BZ566692	pacs2-164
	6	190	8.0	1175	14	CD508153		CD508153	CDA89-C04
c	7	183.4	7.7	712	29	BZ549701		BZ549701	pacs1-60_
	8	181.8	7.6	948	29	BZ553880		BZ553880	pacs1-60_
	9	180.2	7.6	1609	11	AY109160		AY109160	Zea mays
	10	177.2	7.4	1772	11	AK077429		AK077429	Mus muscu
	11	172.8	7.3	1393	11	BC032078		BC032078	Homo sapi
	12	172.4	7.2	1793	11	BC012282		BC012282	Mus muscu
	13	172	7.2	1748	11	AK076982		AK076982	Mus muscu
	14	172	7.2	1752	11	AK010310		AK010310	Mus muscu
	15	167.4	7.0	544	28	AQ989915		AQ989915	Rfc00591
	16	167	7.0	1418	11	AK010644		AK010644	Mus muscu
	17	167	7.0	1438	11	AK075920		AK075920	Mus muscu
	18	163.6	6.9	1165	14	CD507904		CD507904	CDA87-G05
	19	163.6	6.9	1201	9	AL568646		AL568646	AL568646
	20	157	6.6	688	14	CD045220		CD045220	psHB018xI
c	21	156.8	6.6	696	28	BH143507		BH143507	TDGEA79TH
	22	155.6	6.5	786	29	BZ564147		BZ564147	pacs2-164
	23	155.6	6.5	802	13	BU476989		BU476989	603841415
	24	155.2	6.5	972	11	CNS08PRP		BX022817	Single re
	25	153	6.4	1031	11	CNS08DJ2		BX006954	Single re
	26	152.6	6.4	835	29	BZ565507		BZ565507	pacs2-164
	27	152	6.4	1012	13	BU112303		BU112303	603129440
	28	149.4	6.3	1163	14	CD497898		CD497898	CDA30-E05
	29	148.2	6.2	1201	9	AL535247		AL535247	AL535247
	30	148.2	6.2	2972	11	AK031534		AK031534	Mus muscu
	31	147.6	6.2	871	14	CD439282		CD439282	EL01N0523
	32	147	6.2	1033	11	CNS090JP		BX036785	Single re
	33	146.6	6.2	2986	11	AK028274		AK028274	Mus muscu
	34	146.6	6.2	3956	11	BC043699		BC043699	Mus muscu
	35	146.4	6.1	1629	11	AK076509		AK076509	Mus muscu
	36	145.8	6.1	704	13	BU406237		BU406237	603482292
	37	145.8	6.1	832	29	BZ718032		BZ718032	PUBNU85TD
	38	145.8	6.1	1124	13	BX384332		BX384332	BX384332
	39	145.6	6.1	980	11	CNS0941F		BX041311	Single re
c	40	145.6	6.1	1102	29	BZ559358		BZ559358	pacs2-164
	41	145	6.1	2984	11	AK031679		AK031679	Mus muscu
c	42	143.8	6.0	964	11	CNS08V7D		BX029861	Single re
	43	143.8	6.0	1018	11	CNS090FU		BX036646	Single re
	44	143.2	6.0	1151	11	AY105919		AY105919	Zea mays
c	45	142.8	6.0	924	11	CNS09HZH		BX059385	Single re

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 15:25:32 ; Search time 144 Seconds
(without alignments)
7298.147 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	563.8	23.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
2	563.8	23.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
3	465.4	19.5	2100	4	US-09-252-991A-9660	Sequence 9660, Ap
4	465.2	19.5	1785	4	US-09-252-991A-9701	Sequence 9701, Ap
5	357.6	15.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
6	357.6	15.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
7	271.4	11.4	1592	4	US-09-634-238-34	Sequence 34, Appl
8	269.2	11.3	1800	3	US-09-039-773A-1	Sequence 1, Appli
c 9	250.6	10.5	996	4	US-09-252-991A-9594	Sequence 9594, Ap
10	250.2	10.5	1407	4	US-09-252-991A-5967	Sequence 5967, Ap
c 11	250.2	10.5	1620	4	US-09-252-991A-5920	Sequence 5920, Ap

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

```
Run on:      October 14, 2003, 16:30:32 ; Search time 633 Seconds
              (without alignments)
              9760.262 Million cell updates/sec
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Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgccgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2381	100.0	2381	10	US-09-963-790A-1	Appl.	Sequence 1, Appli
2	2377.8	99.9	3309400	10	US-09-738-626-1	Nakagawa	Sequence 1, Appli
3	2126.8	89.3	2196	10	US-09-738-626-1278	"	Sequence 1278, Ap
4	563.8	23.7	75216	15	US-10-080-170-646		Sequence 646, App
5	514.6	21.6	1941	9	US-09-815-242-6214		Sequence 6214, Ap
6	500.2	21.0	1941	9	US-09-815-242-9671		Sequence 9671, Ap
7	468.4	19.7	1704	9	US-09-815-242-7788		Sequence 7788, Ap
8	357.6	15.0	1842	9	US-09-815-242-6893		Sequence 6893, Ap
9	357.6	15.0	1830121	14	US-10-329-960-1		Sequence 1, Appli
c 10	295.8	12.4	640681	10	US-09-790-988-1		Sequence 1, Appli
11	271.4	11.4	1536	10	US-09-971-536-10		Sequence 10, Appl
12	247.4	10.4	2241	14	US-10-156-761-4107		Sequence 4107, Ap
c 13	247.4	10.4	9025608	14	US-10-156-761-1		Sequence 1, Appli
14	235.4	9.9	1575	9	US-09-815-242-9393		Sequence 9393, Ap
15	234.4	9.8	939	10	US-09-974-300-1660		Sequence 1660, Ap
16	234	9.8	1506	14	US-10-156-761-4139		Sequence 4139, Ap
17	234	9.8	9025608	14	US-10-156-761-1		Sequence 1, Appli
18	233	9.8	1618	9	US-09-874-923-9		Sequence 9, Appli
19	233	9.8	1618	10	US-09-991-496-9		Sequence 9, Appli
20	233	9.8	1618	12	US-10-098-732A-68		Sequence 68, Appl
21	230.2	9.7	1530	14	US-10-156-761-4430		Sequence 4430, Ap
c 22	217.8	9.1	38734	11	US-09-373-658-30		Sequence 30, Appl
23	214.4	9.0	1449	10	US-09-974-300-6077		Sequence 6077, Ap
24	214	9.0	1611	9	US-09-815-242-6677		Sequence 6677, Ap
25	212.8	8.9	2293	9	US-09-842-552-85		Sequence 85, Appl
26	212.6	8.9	1272	10	US-09-738-626-859		Sequence 859, App
c 27	212.6	8.9	3309400	10	US-09-738-626-1		Sequence 1, Appli
28	202.4	8.5	2277	14	US-10-156-761-3085		Sequence 3085, Ap
29	200	8.4	1494	14	US-10-156-761-7032		Sequence 7032, Ap
30	187	7.9	1476	10	US-09-732-091-1		Sequence 1, Appli
31	187	7.9	1479	9	US-09-815-242-7211		Sequence 7211, Ap
32	187	7.9	1512	10	US-09-732-091-41		Sequence 41, Appl
33	175.2	7.4	1749	10	US-09-765-231A-14		Sequence 14, Appl
34	174.8	7.3	1227	14	US-10-128-714-2184		Sequence 2184, Ap
35	172.8	7.3	1383	10	US-09-864-864-294		Sequence 294, App
36	172.8	7.3	1383	12	US-10-334-038-15		Sequence 15, Appl
37	168.2	7.1	1266	9	US-09-815-242-7606		Sequence 7606, Ap
38	168	7.1	1823	11	US-09-909-567B-12		Sequence 12, Appl
39	163.8	6.9	1245	10	US-09-938-842A-2339		Sequence 2339, Ap
40	158.4	6.7	2437	10	US-09-833-381-1478		Sequence 1478, Ap
41	158.4	6.7	2437	10	US-09-833-381-1479		Sequence 1479, Ap
42	156.8	6.6	2900	14	US-10-037-270-1045		Sequence 1045, Ap
43	153.4	6.4	1512	10	US-09-880-107-3452		Sequence 3452, Ap
44	152.4	6.4	1682	9	US-09-755-325-7		Sequence 7, Appli
45	152.4	6.4	1682	12	US-10-429-997-7		Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-963-790A-1

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OM nucleic - nucleic search, using sw model

11155.041 Million cell updates/sec

Sequence: 1 caggaaaccccgccaggggtga.....ctctctagtcagagtgcgag 2381

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

```

1:  gb_ba:*
2:  gb_htg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

```

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query		DB	ID	Description
	No.	Score	Match	Length			
	1	2381	100.0	2381	6	AX404864	AX404864 Sequence
	2	2279	95.7	333150	1	AP005277	AP005277 Corynebac
	3	2279	95.7	349980	6	AX127146	AX127146 Sequence
	4	2279	95.7	349980	6	AX127147	AX127147 Sequence
	5	2028	85.2	2196	6	AX121362	AX121362 Sequence
	6	2028	85.2	2196	6	BD163479	BD163479 Novel pol
	7	44	1.8	308650	1	AP005218	AP005218 Corynebac
c	8	26	1.1	10101	1	AE012376	AE012376 Xanthomon
	9	24	1.0	12514	1	AE012011	AE012011 Xanthomon
c	10	24	1.0	320150	1	AP005033	AP005033 Streptomy
	11	23	1.0	10491	1	AE005859	AE005859 Caulobact
c	12	23	1.0	12039	1	AE009534	AE009534 Brucella
	13	23	1.0	12080	1	AE014406	AE014406 Brucella
c	14	23	1.0	109911	2	AC118330_4	Continuation (5 of
	15	23	1.0	190050	1	AL646059	AL646059 Ralstonia
c	16	23	1.0	198050	1	AL646061	AL646061 Ralstonia
c	17	23	1.0	217794	2	AC111124	AC111124 Mus muscu
	18	23	1.0	237801	2	AC137306	AC137306 Rattus no
c	19	23	1.0	238039	2	AC137290	AC137290 Rattus no
c	20	23	1.0	311000	1	SCO939122	AL939122 Streptomy
	21	23	1.0	311583	2	AC105794	AC105794 Rattus no
	22	23	1.0	347660	1	AP002994	AP002994 Mesorhizo
c	23	23	1.0	347660	1	AP002994	AP002994 Mesorhizo
	24	22	0.9	198	6	AX313944	AX313944 Sequence
c	25	22	0.9	301675	1	AP005027	AP005027 Streptomy
	26	21	0.9	28	6	AX404866	AX404866 Sequence
c	27	21	0.9	28	6	AX404867	AX404867 Sequence
c	28	21	0.9	10652	6	AX344648	AX344648 Sequence
c	29	21	0.9	12312	1	AE012307	AE012307 Xanthomon
	30	21	0.9	158944	9	AC096746	AC096746 Homo sapi
	31	21	0.9	159878	2	AC124143	AC124143 Oryza sat
	32	21	0.9	187002	2	AC134483	AC134483 Rattus no
c	33	21	0.9	192234	2	AC132132	AC132132 Mus muscu

OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 22:02:48 ; Search time 634 Seconds
(without alignments)
10137.795 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2381	100.0	2381	24	AAD28043	Corynebacterium gl
	2	2279	95.7	349980	22	AAH68527	C glutamicum codin
	3	2279	95.7	349980	22	AAH68528	C glutamicum codin
	4	2028	85.2	2196	22	AAH66243	C glutamicum codin
	5	1674	70.3	1674	25	ACA00444	C. glutamicum deri
	6	184	7.7	273	25	ACA00443	C. glutamicum deri
	7	22	0.9	198	24	ABN78518	Human helicase-lik
c	8	21	0.9	28	24	AAD28045	Corynebacterium gl
c	9	21	0.9	10652	24	ABN80056	Human chemically m
c	10	20	0.8	1219	23	AAS81866	DNA encoding novel
	11	20	0.8	1266	23	AAS53969	Klebsiella pneumon
c	12	20	0.8	1584	22	AAS57165	cDNA encoding Dros
c	13	20	0.8	1584	23	ABL19907	Drosophila melanog
	14	20	0.8	1584	24	ABN69409	Streptococcus poly
	15	20	0.8	1584	24	ABN70539	Streptococcus poly
	16	20	0.8	1941	23	AAS52577	E. coli DNA for ce
	17	20	0.8	2863	19	AAV38314	Nucleotide sequenc
	18	20	0.8	3020	23	AAS89058	DNA encoding novel
	19	20	0.8	3117	23	AAS73364	DNA encoding novel
	20	20	0.8	3117	23	AAS89055	DNA encoding novel
	21	20	0.8	3117	23	AAS92864	DNA encoding novel
	22	20	0.8	4185	22	AAS57164	DNA encoding Droso
	23	20	0.8	4185	23	ABL19906	Drosophila melanog
c	24	20	0.8	14820	22	AAS46246	DNA encoding novel
c	25	20	0.8	14820	22	AAS46268	DNA encoding novel
	26	20	0.8	68750	21	AAZ55887	Sorangium cellulos
	27	20	0.8	71989	21	AAA29349	Sorangium cellulos
	28	20	0.8	2155561	24	ABN71527	Streptococcus poly
	29	19	0.8	28	24	AAD28044	Corynebacterium gl
c	30	19	0.8	346	21	AAC74485	Human ORFX ORF40 p
c	31	19	0.8	346	24	ABN16048	Human ORFX polynuc
	32	19	0.8	515	24	ABK62676	Rat sequence diffe
c	33	19	0.8	520	19	AAV47569	Leishmania antigen
c	34	19	0.8	520	24	AAF88535	L. major LmgSP1 an
c	35	19	0.8	520	24	AAD40296	Leishmania major L
c	36	19	0.8	520	24	ABK81742	Leishmania antigen
c	37	19	0.8	520	24	AAS96033	Leishmania antigen
	38	19	0.8	557	24	ABK62433	Rat sequence diffe
	39	19	0.8	1371	23	ABL24281	Drosophila melanog
	40	19	0.8	1941	23	AAS56034	Salmonella typhi D
	41	19	0.8	4079	25	ACA56639	Human signalling p
	42	19	0.8	4839	25	ABZ42531	Human neuromedin K
	43	19	0.8	5137	23	ABL24280	Drosophila melanog
c	44	19	0.8	5760	24	ABS78661	M. echinospora DNA
	45	19	0.8	5871	24	ABS78666	S. ghanaensis DNA

ALIGNMENTS

OM nucleic - nucleic search, using sw model

```
Database : EST:*
1:  em_estba:*
2:  em_esthum:*
3:  em_estin:*
4:  em_estmu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
9:  gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
```

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	22	0.9	471	9	AU284741	AU284741 AU284741
	2	22	0.9	562	12	BJ411196	BJ411196 BJ411196
	3	22	0.9	631	9	AU268561	AU268561 AU268561
c	4	22	0.9	660	12	BM634053	BM634053 170006688
c	5	22	0.9	714	12	BM656204	BM656204 170006873
c	6	21	0.9	573	13	BU543982	BU543982 GM880001A
	7	21	0.9	575	29	BZ345001	BZ345001 hr43d08.b
	8	21	0.9	606	12	BM603218	BM603218 170006870
	9	21	0.9	612	28	AZ418854	AZ418854 1M0195C09
	10	21	0.9	715	13	BU634805	BU634805 018D02 In
	11	21	0.9	848	10	BF260369	BF260369 HVSMEf002
c	12	20	0.8	160	28	AZ921472	AZ921472 1006030B0
c	13	20	0.8	275	12	BI674592	BI674592 949022D11
	14	20	0.8	305	9	AA571940	AA571940 vgl2d02.r
c	15	20	0.8	327	28	BH228484	BH228484 1006147C0
c	16	20	0.8	330	28	BH228575	BH228575 1006147F0
c	17	20	0.8	340	28	BH217878	BH217878 1006060G0
	18	20	0.8	344	13	BQ760997	BQ760997 EBro04 SQ
c	19	20	0.8	344	28	BH216414	BH216414 1006042E0
c	20	20	0.8	351	28	BH217881	BH217881 1006060G0
c	21	20	0.8	352	28	AZ921694	AZ921694 1006031E0
c	22	20	0.8	352	28	BH216419	BH216419 1006042E0
c	23	20	0.8	352	28	BH228573	BH228573 1006147F0
c	24	20	0.8	353	28	BH228482	BH228482 1006147C0
c	25	20	0.8	355	28	BH228632	BH228632 1006147H0
	26	20	0.8	363	13	BQ993892	BQ993892 QGF5M01.y
	27	20	0.8	383	9	AW417369	AW417369 53455 MAR
	28	20	0.8	385	9	AW115311	AW115311 rs65e07.y
	29	20	0.8	393	9	AW307746	AW307746 1617 MARC
	30	20	0.8	410	12	BI336407	BI336407 AR095H07S
	31	20	0.8	482	10	BE481452	BE481452 166898 BA
	32	20	0.8	484	12	BM106031	BM106031 509650 MA
c	33	20	0.8	494	28	BH216148	BH216148 1006040F0
	34	20	0.8	497	14	CB287818	CB287818 CMD67 F04
	35	20	0.8	528	10	BE233269	BE233269 139379 MA
	36	20	0.8	532	10	BE234987	BE234987 142387 MA
	37	20	0.8	532	12	BG841542	BG841542 MEST22-H0
	38	20	0.8	554	12	BM132263	BM132263 TgESTzyb0
	39	20	0.8	558	9	AV601072	AV601072 AV601072
	40	20	0.8	562	12	BG834242	BG834242 352389 MA
	41	20	0.8	580	9	AW097037	AW097037 rs31h08.y
c	42	20	0.8	584	14	CD484986	CD484986 3529_1_11
	43	20	0.8	600	14	CB455480	CB455480 712623 MA
	44	20	0.8	608	12	BM078668	BM078668 MEST122-G
	45	20	0.8	614	10	BE205350	BE205350 EST398026

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 19:17:14 ; Search time 144 Seconds
(without alignments)
7298.147 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
	Query	Match	Length	DB	ID		
No.	Score						
c	1	20	0.8	483	4	US-09-252-991A-5687	Sequence 5687, Ap
	2	20	0.8	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
c	3	20	0.8	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
	4	20	0.8	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
	5	20	0.8	68750	3	US-09-335-409-1	Sequence 1, Appli
	6	20	0.8	68750	4	US-09-568-102-1	Sequence 1, Appli
	7	20	0.8	68750	4	US-09-567-969-1	Sequence 1, Appli
	8	20	0.8	68750	4	US-09-568-480-1	Sequence 1, Appli
	9	20	0.8	68750	4	US-09-568-486-1	Sequence 1, Appli
	10	20	0.8	68750	4	US-09-568-472-1	Sequence 1, Appli
	11	20	0.8	68750	4	US-09-567-899-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 23:25:50 ; Search time 632 Seconds
(without alignments)
9775.705 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1731049 seqs, 1297405648 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2381	100.0	2381	10	US-09-963-790A-1	Sequence 1, Appli	
2	2279	95.7	3309400	10	US-09-738-626-1	Sequence 1, Appli	
3	2028	85.2	2196	10	US-09-738-626-1278	Sequence 1278, Ap	
4	24	1.0	2064	14	US-10-156-761-2902	Sequence 2902, Ap	
5	24	1.0	125746	14	US-10-156-761-15102	Sequence 15102, A	
c 6	24	1.0	9025608	14	US-10-156-761-1	Sequence 1, Appli	
7	22	0.9	603	14	US-10-156-761-1568	Sequence 1568, Ap	
8	21	0.9	28	10	US-09-963-790A-3	Sequence 3, Appli	
c 9	21	0.9	28	10	US-09-963-790A-4	Sequence 4, Appli	
c 10	20	0.8	503	11	US-09-918-995-34274	Sequence 34274, A	
11	20	0.8	1266	9	US-09-815-242-7606	Sequence 7606, Ap	
c 12	20	0.8	1584	14	US-10-270-333-140	Sequence 140, App	
13	20	0.8	1941	9	US-09-815-242-6214	Sequence 6214, Ap	
14	20	0.8	4185	14	US-10-270-333-139	Sequence 139, App	
15	20	0.8	68750	13	US-10-014-717-1	Sequence 1, Appli	
16	19	0.8	480	10	US-09-991-496-132	Sequence 132, App	
17	19	0.8	515	10	US-09-917-800A-583	Sequence 583, App	
c 18	19	0.8	520	9	US-09-874-923-29	Sequence 29, Appl	
c 19	19	0.8	520	10	US-09-991-496-29	Sequence 29, Appl	
20	19	0.8	522	14	US-10-156-761-2688	Sequence 2688, Ap	
21	19	0.8	546	14	US-10-156-761-1619	Sequence 1619, Ap	
22	19	0.8	557	10	US-09-917-800A-340	Sequence 340, App	
23	19	0.8	561	14	US-10-156-761-3799	Sequence 3799, Ap	
c 24	19	0.8	1137	14	US-10-156-761-6123	Sequence 6123, Ap	
c 25	19	0.8	1495	10	US-09-991-496-133	Sequence 133, App	
26	19	0.8	1941	9	US-09-815-242-9671	Sequence 9671, Ap	
c 27	19	0.8	2613	14	US-10-156-761-6694	Sequence 6694, Ap	
28	19	0.8	4839	14	US-10-225-567A-544	Sequence 544, App	
29	19	0.8	75216	15	US-10-080-170-646	Sequence 646, App	
30	19	0.8	9025608	14	US-10-156-761-1	Sequence 1, Appli	
c 31	18	0.8	273	9	US-09-294-093B-2452	Sequence 2452, Ap	
32	18	0.8	287	9	US-09-294-093B-2110	Sequence 2110, Ap	
33	18	0.8	453	13	US-10-027-632-45454	Sequence 45454, A	
c 34	18	0.8	511	10	US-09-783-590-5786	Sequence 5786, Ap	
35	18	0.8	576	14	US-10-156-761-2684	Sequence 2684, Ap	
36	18	0.8	577	13	US-10-027-632-60237	Sequence 60237, A	
37	18	0.8	577	13	US-10-027-632-298225	Sequence 298225,	
38	18	0.8	603	14	US-10-156-761-6940	Sequence 6940, Ap	
39	18	0.8	624	14	US-10-156-761-2946	Sequence 2946, Ap	
40	18	0.8	630	13	US-10-027-632-85667	Sequence 85667, A	
41	18	0.8	630	13	US-10-027-632-109733	Sequence 109733,	
42	18	0.8	630	13	US-10-027-632-315189	Sequence 315189,	
43	18	0.8	630	13	US-10-027-632-315190	Sequence 315190,	
c 44	18	0.8	877	13	US-10-027-632-10098	Sequence 10098, A	
45	18	0.8	966	14	US-10-156-761-3002	Sequence 3002, Ap	

ALIGNMENTS

RESULT 1
US-09-963-790A-1

OM protein - nucleic search, using frame plus p2n model

```
Title:          US-09-963-790A-2
Perfect score:  3190
Sequence:       1 MPERVLDVAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624
```

Searched: 2888711 seqs, 20454813386 residues

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Command line parameters:

Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152711_1464/app_query.fasta_1.77

```
Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
```

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	3187	99.9	2381	6	AX404864			AX404864 Sequence
	2	3180	99.7	2196	6	AX121362			AX121362 Sequence
	3	3180	99.7	2196	6	BD163479			BD163479 Novel pol
	4	3180	99.7	333150	1	AP005277			AP005277 Corynebac
	5	3180	99.7	349980	6	AX127146			AX127146 Sequence
	6	3180	99.7	349980	6	AX127147			AX127147 Sequence
	7	2825	88.6	308650	1	AP005218			AP005218 Corynebac
	8	1669.5	52.3	299450	1	BX248338			BX248338 Mycobacte
	9	1667.5	52.3	17916	1	AE007004			AE007004 Mycobacte
	10	1667.5	52.3	36030	1	MTCY50			Z77137 Mycobacteri
	11	1667.5	52.3	75216	6	AX704275			AX704275 Sequence
c	12	1587	49.7	12009	1	AE011922			AE011922 Xanthomon
c	13	1584.5	49.7	10101	1	AE012376			AE012376 Xanthomon
	14	1527	47.9	11785	1	AE012833			AE012833 Chlorobiu
c	15	1520	47.6	300029	1	AE012553			AE012553 Xylella f
c	16	1511.5	47.4	12008	1	AE003878			AE003878 Xylella f

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

```
Run on:      October 15, 2003, 09:38:57 ; Search time 447 Seconds
              (without alignments)
              3768.343 Million cell updates/sec
```

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVG YETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop 6.0 , Delext 7.0
```

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlh
```

Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152711_1428/app_query.fasta_1.77
5

```
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790 @CGN_1_1_0 @runat_14102003_152711_1428 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
```

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	3187	99.9	2381	24	AAD28043	Corynebacterium gl
	2	3180	99.7	2196	22	AAH66243	C glutamicum codin
	3	3180	99.7	349980	22	AAH68527	C glutamicum codin
	4	3180	99.7	349980	22	AAH68528	C glutamicum codin
	5	2865	89.8	1674	25	ACA00444	C. glutamicum deri
	6	1667.5	52.3	75216	24	ABX09141	Mycobacterium tube
	7	1667.5	52.3	4403765	22	AAI99683	Mycobacterium tube
	8	1667.5	52.3	4411529	22	AAI99682	Mycobacterium tube
	9	1423.5	44.6	1941	23	AAS52577	E. coli DNA for ce
c	10	1423.5	44.6	14820	22	AAS46246	DNA encoding novel
c	11	1423.5	44.6	14820	22	AAS46268	DNA encoding novel
	12	1422.5	44.6	1941	23	AAS56034	Salmonella typhi D
	13	1391.5	43.6	2863	19	AAV38314	Nucleotide sequenc
	14	1333.5	41.8	1842	23	AAS53256	Haemophilus influe
	15	1333.5	41.8	1830121	17	AAT42063	Haemophilus influe
c	16	1300	40.8	640681	24	ABA92787	Buchnera sp. genom
	17	1200.5	37.6	1704	23	AAS54151	Pseudomonas aerugi
	18	1118	35.0	3020	23	AAS89058	DNA encoding novel
c	19	1113	34.9	1219	23	AAS81866	DNA encoding novel
	20	980	30.7	1449	24	ABK78786	Bacillus clausii g
	21	974	30.5	1584	24	ABN69409	Streptococcus poly
	22	974	30.5	1584	24	ABN70539	Streptococcus poly
	23	974	30.5	2155561	24	ABN71527	Streptococcus poly
	24	962.5	30.2	2365589	24	ABA90521	Genomic sequence o
	25	958.5	30.0	2944528	24	ABA03041	Listeria monocytog
	26	956.5	30.0	1617	24	ABN69410	Streptococcus poly
	27	952.5	29.9	5738	24	ABQ70978	Listeria monocytog
	28	950	29.8	1163020	24	ABQ67197	Listeria innocua c
	29	950	29.8	3011208	24	ABQ69245	Listeria innocua D
	30	912.5	28.6	1611	23	AAS53040	Enterococcus faeca
	31	906	28.4	1572	25	ABX07336	S. pneumoniae type
	32	906	28.4	1575	23	AAS55756	Streptococcus pneu

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 09:38:44 ; Search time 3488 Seconds
(without alignments)
4348.048 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152712_1487/app_query.fasta_1.77
5

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790 @CGN_1_1_2810 @runat_14102003_152712_1487 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*


```

11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	922.5	28.9	3539	28	BH770982		BH770982	LLMGtag70
	2	703.5	22.1	2376	11	AK030239		AK030239	Mus muscu
	3	703.5	22.1	2517	11	BC049906		BC049906	Mus muscu
	4	703.5	22.1	2638	11	AK041281		AK041281	Mus muscu
	5	680	21.3	2756	11	AK010281		AK010281	Mus muscu
	6	680	21.3	4723	11	BC043655		BC043655	Mus muscu
	7	674.5	21.1	1393	11	BC032078		BC032078	Homo sapi
	8	674.5	21.1	1772	11	AK077429		AK077429	Mus muscu
	9	674.5	21.1	1793	11	BC012282		BC012282	Mus muscu
	10	671.5	21.1	3212	11	AK029542		AK029542	Mus muscu
	11	669.5	21.0	1629	11	AK076509		AK076509	Mus muscu
	12	669	21.0	1438	11	AK075920		AK075920	Mus muscu
	13	668	20.9	2321	11	BC046554		BC046554	Mus muscu
	14	668	20.9	2329	11	AK088887		AK088887	Mus muscu
	15	664.5	20.8	4014	11	AK049311		AK049311	Mus muscu
	16	664	20.8	3313	11	BC009432		BC009432	Homo sapi
	17	663.5	20.8	1748	11	AK076982		AK076982	Mus muscu
	18	663.5	20.8	1752	11	AK010310		AK010310	Mus muscu
	19	660	20.7	2329	11	AK044792		AK044792	Mus muscu
	20	658	20.6	4626	11	BC007668		BC007668	Homo sapi
	21	651	20.4	1609	11	AY109160		AY109160	Zea mays
	22	649.5	20.4	1929	11	AY104966		AY104966	Zea mays
	23	641.5	20.1	1418	11	AK010644		AK010644	Mus muscu
	24	641	20.1	1902	11	BC006469		BC006469	Homo sapi
	25	638	20.0	3031	11	BC051046		BC051046	Mus muscu
	26	625	19.6	2338	11	AK076018		AK076018	Mus muscu
	27	619.5	19.4	1443	12	BM321064		BM321064	rockefell
	28	619	19.4	1201	9	AL568646		AL568646	AL568646

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      October 15, 2003, 12:06:29 ; Search time 100 Seconds
              (without alignments)
              2754.231 Million cell updates/sec
```

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
```

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlh
```

Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152709_1336/app_query.fasta_1.775

```
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09963790_CGN_1_1_56_runat_14102003_152709_1336 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      Issued_Patents_NA:*
1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1667.5	52.3	4403765	3	US-09-103-840A-2			Sequence 2, Appli
	2	1667.5	52.3	4411529	3	US-09-103-840A-1			Sequence 1, Appli
	3	1333.5	41.8	1830121	4	US-09-557-884-1			Sequence 1, Appli
	4	1333.5	41.8	1830121	4	US-09-643-990A-1			Sequence 1, Appli
	5	1201	37.6	2100	4	US-09-252-991A-9660			Sequence 9660, Ap
	6	1200.5	37.6	1785	4	US-09-252-991A-9701			Sequence 9701, Ap
c	7	906	28.4	3230	4	US-08-961-527-203			Sequence 203, App
	8	904	28.3	1533	4	US-09-107-532A-2328			Sequence 2328, Ap
	9	897.5	28.1	1800	3	US-09-039-773A-1			Sequence 1, Appli
	10	895	28.1	1592	4	US-09-634-238-34			Sequence 34, Appl
	11	848	26.6	1587	4	US-09-134-001C-1425			Sequence 1425, Ap
	12	790.5	24.8	1941	4	US-09-328-352-1891			Sequence 1891, Ap
	13	786	24.6	1407	4	US-09-252-991A-5967			Sequence 5967, Ap
c	14	786	24.6	1620	4	US-09-252-991A-5920			Sequence 5920, Ap
c	15	783	24.5	4774	4	US-09-221-017B-1			Sequence 1, Appli
	16	769.5	24.1	1664976	4	US-08-916-421B-1			Sequence 1, Appli
	17	723.5	22.7	1488	4	US-09-252-991A-421			Sequence 421, App
	18	716.5	22.5	1374	3	US-08-929-738-1			Sequence 1, Appli
	19	716.5	22.5	1614	3	US-08-929-738-2			Sequence 2, Appli
	20	687	21.5	3288	4	US-09-844-521-3			Sequence 3, Appli
	21	687	21.5	3304	4	US-09-620-312D-105			Sequence 105, App
	22	685	21.5	1383	4	US-09-252-991A-5684			Sequence 5684, Ap
c	23	685	21.5	1557	4	US-09-252-991A-5539			Sequence 5539, Ap
c	24	683	21.4	1830121	4	US-09-557-884-1			Sequence 1, Appli
c	25	683	21.4	1830121	4	US-09-643-990A-1			Sequence 1, Appli
	26	676	21.2	1682	3	US-09-318-443-7			Sequence 7, Appli
	27	673	21.1	1536	3	US-09-318-443-5			Sequence 5, Appli
	28	663.5	20.8	1254	5	PCT-US96-05320A-894			Sequence 894, App
	29	662	20.8	1245	3	US-09-318-443-1			Sequence 1, Appli
	30	661	20.7	2319	3	US-09-058-489-90			Sequence 90, Appl
	31	661	20.7	4416	3	US-09-058-489-17			Sequence 17, Appl
	32	658.5	20.6	3408	3	US-09-058-489-14			Sequence 14, Appl
	33	658.5	20.6	5322	3	US-09-058-489-13			Sequence 13, Appl
	34	653	20.5	3825	3	US-09-208-742-3			Sequence 3, Appli
c	35	652	20.4	1602	4	US-09-252-991A-3776			Sequence 3776, Ap
	36	652	20.4	1755	4	US-09-252-991A-3588			Sequence 3588, Ap
	37	652	20.4	1867	2	US-08-607-509-3			Sequence 3, Appli
	38	652	20.4	1867	2	US-08-634-642-3			Sequence 3, Appli
	39	652	20.4	1867	3	US-08-989-370-3			Sequence 3, Appli
	40	649	20.3	3347	4	US-09-702-705-318			Sequence 318, App
	41	649	20.3	3347	4	US-09-736-457-318			Sequence 318, App
	42	645.5	20.2	1116	4	US-09-252-991A-5946			Sequence 5946, Ap
	43	644	20.2	1281	4	US-09-252-991A-3691			Sequence 3691, Ap
	44	640	20.1	1618	2	US-08-533-669A-9			Sequence 9, Appli
	45	640	20.1	1618	2	US-08-607-509-1			Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-103-840A-2

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 11:02:43 ; Search time 1123 Seconds
(without alignments)
1441.819 Million cell updates/sec

Title: US-09-963-790A-2
Perfect score: 3190
Sequence: 1 MPERVLDAVRKVGYETPSPI.....RGRDDRGDRGGRGGYRGGRD 624

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-

Q=/cgn2_1/USPTO_spool/US09963790/runat_14102003_152710_1373/app_query.fasta_1.77
5

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09963790 @CGN_1_1_271 @runat_14102003_152710_1373
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				ID	Description
	No.	Score	Match	Length	DB					
	1	3187	99.9	2381	10	US-09-963-790A-1				Sequence 1, Appli
	2	3180	99.7	2196	10	US-09-738-626-1278				Sequence 1278, Ap
	3	3180	99.7	3309400	10	US-09-738-626-1				Sequence 1, Appli
	4	1667.5	52.3	75216	15	US-10-080-170-646				Sequence 646, App
	5	1423.5	44.6	1941	9	US-09-815-242-6214				Sequence 6214, Ap
	6	1422.5	44.6	1941	9	US-09-815-242-9671				Sequence 9671, Ap
	7	1333.5	41.8	1842	9	US-09-815-242-6893				Sequence 6893, Ap
	8	1333.5	41.8	1830121	14	US-10-329-960-1				Sequence 1, Appli
c	9	1300	40.8	640681	10	US-09-790-988-1				Sequence 1, Appli
	10	1200.5	37.6	1704	9	US-09-815-242-7788				Sequence 7788, Ap
	11	980	30.7	1449	10	US-09-974-300-6077				Sequence 6077, Ap
	12	912.5	28.6	1611	9	US-09-815-242-6677				Sequence 6677, Ap
	13	906	28.4	1575	9	US-09-815-242-9393				Sequence 9393, Ap
	14	898	28.2	1536	10	US-09-971-536-10				Sequence 10, Appl
	15	866.5	27.2	2241	14	US-10-156-761-4107				Sequence 4107, Ap
c	16	866.5	27.2	9025608	14	US-10-156-761-1				Sequence 1, Appli
	17	841	26.4	2293	9	US-09-842-552-85				Sequence 85, Appl
	18	840	26.3	1677	10	US-09-925-637-73				Sequence 73, Appl
	19	840	26.3	1677	14	US-10-084-205-73				Sequence 73, Appl
	20	839	26.3	1530	9	US-09-815-242-4201				Sequence 4201, Ap
	21	836	26.2	9025608	14	US-10-156-761-1				Sequence 1, Appli
	22	835	26.2	1464	9	US-09-815-242-8299				Sequence 8299, Ap
	23	835	26.2	1464	9	US-09-815-242-8893				Sequence 8893, Ap
	24	823	25.8	2799	9	US-09-902-627-2				Sequence 2, Appli
	25	822	25.8	7363	8	US-08-781-986A-19				Sequence 19, Appl
	26	812.5	25.5	1476	10	US-09-732-091-1				Sequence 1, Appli
	27	812.5	25.5	1479	9	US-09-815-242-7211				Sequence 7211, Ap
	28	812.5	25.5	1512	10	US-09-732-091-41				Sequence 41, Appl
	29	804	25.2	2277	14	US-10-156-761-3085				Sequence 3085, Ap
	30	714	22.4	1833	10	US-09-938-842A-1839				Sequence 1839, Ap
	31	710.5	22.3	1272	10	US-09-738-626-859				Sequence 859, App
c	32	710.5	22.3	3309400	10	US-09-738-626-1				Sequence 1, Appli
	33	704	22.1	1860	10	US-09-938-842A-699				Sequence 699, App
	34	691.5	21.7	1227	14	US-10-128-714-2184				Sequence 2184, Ap
	35	690	21.6	3501	10	US-09-938-842A-13				Sequence 13, Appl
	36	689.5	21.6	3352	14	US-10-128-714-184				Sequence 184, App
	37	687	21.5	3304	14	US-10-037-270-105				Sequence 105, App
	38	687	21.5	4689	9	US-09-895-652-10				Sequence 10, Appl
	39	684.5	21.5	4105	14	US-10-128-714-551				Sequence 551, App
	40	684.5	21.5	4105	14	US-10-128-714-5551				Sequence 5551, Ap